



-1-

SEQUENCE LISTING

<110> Umana, Pablo
Bruenker, Peter
Ferrara, Claudia
Suter, Tobias

<120> Fusion Constructs and Use of Same to Produce Antibodies with Increased Fc Receptor Binding Affinity and Effector Function

<130> 1975.0180003

<140> US 10/761,435
<141> 2004-01/22

<150> US 60/441,307
<151> 2003-01-22

<150> US 60/491,254
<151> 2003-07-31

<150> US 60/495,142
<151> 2003-08-15

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 11
<212> PRT
<213> Unknown

<220>
<223> c-myc epitope tag

<400> 1

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-177 PCR primer

<400> 2
gctgtgcct gtgacccccc cgccccctgct ccagccactg tcccc 45

<210> 3
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-178 PCR primer

<400> 3
gaaggtttct ccagcatcct ggtacc 26

<210> 4
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-179 PCR primer

<400> 4
ctgaggcgcg ccgccaccat gctgaagaag cagtctgcag ggc 43

<210> 5
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-180 PCR primer

<400> 5
ggggacagtg gctggaggcag gggcgcgcccc gtcacaggca cacgcggc 48

<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-252 PCR primer

<400> 6
gctaggccgg ccgccaccat gaagttaagc cgccagttca ccgtgttcgg 50

<210> 7
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-253 PCR primer

<400> 7
ggggacagtg gctggaggcag gggtgagcca gcaccttggc tgaaattgct ttgtgaactt 60
ttcgg 65

<210> 8
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-254 PCR primer

<400> 8
tccgaaaagt tcacaaagca atttcagcca aggtgctggc tcacccctgc tccagccact 60
gtcccc 66

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-255 PCR primer

<400> 9
atgccgcata ggccctccgag caggacc 29

<210> 10
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-261 PCR primer

<400> 10
gctaaatatt gaattccctt tatgtgtaac tcttggtga agc 43

<210> 11
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> GAB-262 PCR primer

<400> 11
tagcaatatt gaattcgcag gaaaaggaca agcagcgaaa attcacgc 48

<210> 12
<211> 1715
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of GnTI-GnTIII

<400> 12
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgctctacc ttagtgcgtt ccggggtcac tttagactacc ccaggaaccc ggcgcgcgag 120
ggctccttcc ctcaggggcca gctctcaatg ttgcaagaaa aaatagacca ttggagcgt 180
ttgcttagctg agaataatga gatcatctca aatatttagag actcagtcatttcaatgg 240
gagtctgtgg aggtatgtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300
ccccctgctcc agccactgtc ccctagcaag gccaccgaag aactgcacccg ggtggacttc 360

gtgttgcgg aggacaccac agagtattt gtgcgcacca aagctggcg	420
aaaccaggta ccaggatgct ggagaaacct tctccaggc gcacagagga	480
gtggctgagg ggtcctcggt ccggggtcct gctcgaggc ctatgcggca	540
gcacgggagc gcctgggagg cggggcact aggcgcaagt gggttgagtg	600
ccaggctggc acgggcccag ctgcggggtg cccactgtgg tccagtattc	660
accaggagc gcctggtacc cagggaggtg ccgaggcggg ttatcaacgc	720
aaccatgagt tcgacactgct ggatgtgcgc ttccatgagc tggcgatgt	780
tttgtggct gcgaatccaa tttcacccgc tacggggagc ctggccgct	840
gagatgctga ccaatggcac ctgcagatc atccgcaca aggtgctcta	900
gaccacttcc cacctggtgg ccgtcaggac ggctggattg cagacgacta	960
ttccctaccc agatgggtgt ctccgcctg cgcaacctgc gacctgatga	1020
atcgacgacg cggacgagat ccctgcgcgt gatggtgtgc tgccctcaa	1080
ggctggacag agcccttcgc cttccatatg cgcaagtccc tgtatggttt	1140
caaccaggca cacggaggtg gtgtcaggct gcaccattga catgctgcag	1200
ggctggacgg catccgcctg cggccgcgtc agtactacac catgccaac	1260
atgagaaccg caccggccac atcctagtgc agtggctct cggcagcccc	1320
cgggctggca ctgctccctgg tgccctcacac ccgagggcat ctacttcaa	1380
cccagaatgg tgacttcccc cgctggggtg actacgagga caagagggac	1440
tccgaagctt gattcgcact gggggatggt tcgacggcac gcagcaggag	1500
cagaccccg tgaacacatg tatgctccta agtacctgct caagaactat	1560
gctacttgct cgaaaatccc taccgggagc ccaagagcac tgttaggggt	1620
accagggctc agacggaagg tcatctgctg tcagggcaa gttggataca	1680
cggAACAGAA actgatctct gaagaggacc tgtag	1715

<210> 13
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of GnTI-GnTIII
<400> 13

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp

20

25

30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys Ala Thr
100 105 110

Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr Thr Glu
115 120 125

Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro Gly Thr
130 135 140

Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys Thr Lys
145 150 155 160

Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro Met Arg
165 170 175

His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr Arg Arg
180 185 190

Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro Ser Cys
195 200 205

Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys Glu Arg
210 215 220

Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile Asn Ile
225 230 235 240

Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu Gly Asp
245 250 255

Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala Tyr Gly
260 265 270

Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe
275 280 285

Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro
290 295 300

Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr
305 310 315 320

Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp
325 330 335

Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly
340 345 350

Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe
355 360 365

His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr
370 375 380

Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr
385 390 395 400

Gly Leu Asp Gly Ile Arg Leu Arg Arg Gln Tyr Tyr Thr Met Pro
405 410 415

Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp
420 425 430

Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys
435 440 445

Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly
450 455 460

Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr
465 470 475 480

Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln
485 490 495

Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr
500 505 510

Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr
515 520 525

Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser
530 535 540

Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly
545 550 555 560

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 14
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GnTIII

<400> 14
atgctgaaga agcagtctgc agggcttgtg ctgtggggcg ctatcctctt tgtggcctgg 60
aatgccctgc tgctcctctt cttctggacg cgcccagcac ctggcaggcc accctcagtc 120
agcgctctcg atggcgaccc cgccagcctc acccgggaag tgattcgctt ggcccaagac 180
gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcggga tggccctgtcg 240
agccagcggg ggagggtgcc caccgcggcc cctcccgccc agccgcgtgt gcctgtgacc 300
cccgcgcccc tgctccagcc actgtcccct agcaaggcca ccgaagaact gcaccgggtg 360
gacttcgtgt tgccggagga caccacagag tattttgtgc gcaccaaagc tggcgggtgt 420
tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag 480
accaagggtgg ctgaggggtc ctcggtccgg ggtcctgctc ggaggcctat gccgcgtgt 540
ttgagtgcac gggagcgcct gggaggccgg ggcacttaggc gcaagtgggt tgagtgtgt 600
tgccctgccag gctggcacgg gcccagctgc ggggtgccca ctgtggtcca gtattccaac 660
ctgcccacca aggagcgcct ggtacccagg gaggtgccga ggcgggttat caacgcacatc 720
aacatcaacc atgagttcga cctgctggat gtgcgttcc atgagctggg cgatgttgt 780
gacgcctttg tggctgcga atccaatttc accgcctacg gggagcctcg gccgctcaag 840
ttccgagaga tgctgaccaa tggcaccttc gagtacatcc gccacaaggt gctctacgtc 900
ttcctggacc acttcccacc tggtgccgt caggacggct ggattgcaga cgactacctg 960
cgtaccttcc tcacccagga tggtgtctcc cgccctgcgca acctgcgacc tgatgacgtc 1020
tttatcatcg acgacgcgga cgagatccct ggcgcgtatg gtgtgctgtt cctcaagctc 1080
tacgatggct ggacagagcc cttcgcccttc catatgcgca agtccctgtta tggtttctt 1140
tggaaagcaac caggcacact ggaggtggtg tcaggctgca ccattgacat gctgcaggct 1200

gtgtatgggc tggacggcat ccgcctgcgc cgccgtcagt actacaccat gcccaactt	1260
cgacagtatg agaaccgcac cggccacatc ctagtgcagt ggtctctcgg cagccccctg	1320
cacttcgcgg gctggcactg ctccctggtgc ttcacacccg agggcatcta ctcaaactc	1380
gtgtcggccc agaatggtga cttcccccgc tgggtgact acgaggacaa gagggacctc	1440
aattacatcc gaagcttgat tcgcactggg ggtgggttcg acggcacgca gcaggagtac	1500
cctcctgcag accccagtga acacatgtat gctcctaagt acctgctcaa gaactatgac	1560
cagttccgct acttgctcga aaatccctac cgggagccca agagcactgt agagggtggg	1620
cggcggAACCC agggctcaga cggaaaggta tctgctgtca gggcaagtt ggataacaacg	1680
gaggggccgg aacagaaaact gatctctgaa gaggacctgt ag	1722

<210> 15
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GnTIII fusion

<400> 15

Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu			
1	5	10	15

Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro		
20	25	30

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala		
35	40	45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu		
50	55	60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser			
65	70	75	80

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg		
85	90	95

Val Pro Val Thr Pro Ala Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys		
100	105	110

Ala Thr Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr		
115	120	125

Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro

130

135

140

Gly Thr Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys
145 150 155 160

Thr Lys Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro
165 170 175

Met Arg His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr
180 185 190

Arg Arg Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro
195 200 205

Ser Cys Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys
210 215 220

Glu Arg Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile
225 230 235 240

Asn Ile Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu
245 250 255

Gly Asp Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala
260 265 270

Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly
275 280 285

Thr Phe Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His
290 295 300

Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu
305 310 315 320

Arg Thr Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg
325 330 335

Pro Asp Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg
340 345 350

Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe
355 360 365

Ala Phe His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro
370 375 380

-10-

Gly Thr Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala
385 390 395 400

Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr
405 410 415

Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val
420 425 430

Gln Trp Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser
435 440 445

Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln
450 455 460

Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu
465 470 475 480

Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr
485 490 495

Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro
500 505 510

Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn
515 520 525

Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln
530 535 540

Gly Ser Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr
545 550 555 560

Glu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
565 570

<210> 16
<211> 398
<212> PRT
<213> Unknown

<220>
<223> GalT amino acid sequence from pBlueGalT

<400> 16

Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
1 5 10 15

Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
20 25 30

His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
35 40 45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
50 55 60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
65 70 75 80

Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln Pro Arg Pro
85 90 95

Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly Pro Ala Ser
100 105 110

Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu Ser Leu Pro
115 120 125

Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met Leu Ile Glu
130 135 140

Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln Asn Pro Asn
145 150 155 160

Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val Ser Pro His
165 170 175

Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu His Leu Lys
180 185 190

Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln Gln Leu Asp
195 200 205

Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile Phe Asn Arg
210 215 220

Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys Asp Tyr Asp
225 230 235 240

Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro Met Asn Asp
245 250 255

His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile Ser Val Ala
260 265 270

Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr Phe Gly Gly
275 280 285

Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn Gly Phe Pro
290 295 300

Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile Phe Asn Arg
305 310 315 320

Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala Val Val Gly
325 330 335

Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn Glu Pro Asn
340 345 350

Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr Met Leu Ser
355 360 365

Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val Gln Arg Tyr
370 375 380

Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro Ser
385 390 395

<210> 17
<211> 3435
<212> DNA
<213> Homo sapiens

<400> 17
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgccttacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgcgcgag 120
ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
ttgctagctg agaataatga gatcatctca aatatttagag actcagtcat caatttgagt 240
gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300
catcttctgc cctcacaatt atccctctca gttgacactg cagactgtct gtttgcattca 360
caaagtggaa gtcacaattc agatgtgcag atgttggatg tttacagtct aatttctttt 420
gacaatccag atggtggagt ttggaagcaa ggatttgaca ttacttatga atctaatgaa 480
tgggacactg aacccttca agtcttgcgt gtgcctcatt cccataacga cccaggttgg 540
ttgaagactt tcaatgacta cttagagac aagactcagt atattttaa taacatggtc 600
ctaaagctga aagaagactc acggaggaag tttatgggt ctgagatctc ttaccttca 660
aagtggtggg atattataga tattcagaag aaggatgctg taaaagttt aatagaaaaat 720

ggtcagcttg aaattgtgac aggtggctgg gttatgcctg atgaagctac tccacattat	780
tttgccttaa ttgatcaact aattgaagga catcagtggc tggaaaataa tataggagtg	840
aaacctcggt ccggctgggc tattgatccc tttggacact caccaacaat ggcttatctt	900
ctaaaccgtg ctggactttc tcacatgctt atccagagag ttcattatgc agttaaaaaaa	960
cactttgcac tgcataaaac attggagttt ttttgagac agaattggga tctggatct	1020
gtcacagata ttttatgcc a catgatgccc ttctacagct atgacatccc tcacacttgt	1080
ggacctgatc ctaaaatatg ctgccagttt gattttaaac gtcttcctgg aggtagattt	1140
ggttgcctt ggggagtccc cccagaaaca atacatcctg gaaatgtcca aagcaggcgt	1200
cggatgctac tagatcagta ccgaaagaag tcaaagcttt ttcgtaccaa agttctcctg	1260
gctccactag gagatgattt ccgctactgt gaatacacgg aatgggattt acagtttaag	1320
aattatcagc agcttttga ttatataat tctcagtc a agtttaaagt taagatacag	1380
tttggaaactt tatcagattt tttgatgcg ctggataaag cagatgaaac tcagagagac	1440
aaggccagt cgatgttccc tgtttaagt ggagatttt tcacttatgc cgatcgagat	1500
gatcattact ggagtggcta ttttacatcc agacccttt acaaacgaat ggacagaatc	1560
atggaatctc attaagggc tgctgaaatt cttaacttatt tcgccccgt acaagctcac	1620
aaatacaaga taaataaatt tctctcatca tcactttaca cggcaactgac agaagccaga	1680
aggaatttgg gactgttca acatcatgat gctatcacag gaactgcaaa agactgggtg	1740
gttgcgttattt atggtaaccag acttttcatt tcgttaatgg ttttgagaa gataattgga	1800
aattctgcattt tttgaaggac aaactcacat acgactctt ctctcctgat	1860
accttcctgg agatggattt gaaacaaaaa tcacaagatt ctctgccaca aaaaaatata	1920
ataaggctga gtgcggagcc aaggtacattt gtggctata atcctttaga acaagaccga	1980
atctcggttgg tctcagtcata tgtgagttcc ccgacagtgc aagtgttctc tgcttcagga	2040
aaacctgtgg aagttcaagt cagcgcagtt tggatacag caaatactat ttcaaaaaca	2100
gcctatgaga tctctttcg agcacatata ccggcattgg gactgaaagt gtataagatt	2160
tttggaaatcg caagttcaaa ttcacattt gctgattatg tcttgtataa gaataaaagta	2220
gaagatagcg gaattttcac cataaagaat atgataaata ctgaagaagg tataacacta	2280
gagaactcct ttgtttact tcggtttgat caaactggac ttatgaagca aatgatgact	2340
aaagaagatg gttaaacacca tgaagtaaat gtgcattttt catggatgg aaccacaatt	2400
aaaagagaca aaagtggtgc ctacctcttc ttacctgatg gtaatgccaa gccttatgtt	2460
tacacaacac cgcccttgc cagagtgaca catggaagga tttattcgga agtgacttgc	2520
ttttttgacc atgttactca tagagtccga ctataccaca tacagggaaat agaaggacag	2580

tctgtggaag tttccaatat tgtggacatc cgaaaagtat ataaccgtga gattgcaatg	2640
aaaatttctt ctgatataaa aagccaaaat agattttata ctgacctaaa tgggtaccag	2700
attcaaccta gaatgacact gagcaaattg cctcttcaag caaatgtcta tc(ccatgacc	2760
acaatggcct atatccagga tgccaaacat cgtttgacac tgctctgc tcagtctta	2820
ggggtttcga gtttgaatag tggtcagatt gaagttatca tggatcgaag actcatgcaa	2880
gatgataatc gtggccttga gcaaggtatc caggataaca agattacagc taatctattt	2940
cgaatactac tagaaaaaaag aagtgctgtt aatacggaa aagaaaagaa gtcggtcagt	3000
tatccttctc tccttagcca cataacttct tctctcatga atcatccagt cattccaatg	3060
gcaaataagt tcttcacc tacccttgag ctgcaaggtg aattctctcc attacagtca	3120
tctttgcctt gtgacattca tctggtaat ttgagaacaa tacagtcaaa ggtgggcaat	3180
gggcactcca atgaggcagc cttgatcctc cacagaaaag ggtttgattg tcggttctct	3240
agcaaaggca cagggctgtt ttgttctact actcagggaa agatattggt acagaaaactt	3300
ttaaacaagt ttattgtcga aagtctcaca cttcatcac tatccttgat gcattcacct	3360
cccgccactc agaatataag tgagatcaac ttgagtccaa tggaaatcag cacattccga	3420
atccagttga ggtga	3435

<210> 18
<211> 1144
<212> PRT
<213> Homo sapiens

<400> 18
Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
1 5 10 15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
85 90 95

Gly Ala Gly Ser His Leu Leu Pro Ser Gln Leu Ser Leu Ser Val Asp
100 105 110

Thr Ala Asp Cys Leu Phe Ala Ser Gln Ser Gly Ser His Asn Ser Asp
115 120 125

Val Gln Met Leu Asp Val Tyr Ser Leu Ile Ser Phe Asp Asn Pro Asp
130 135 140

Gly Gly Val Trp Lys Gln Gly Phe Asp Ile Thr Tyr Glu Ser Asn Glu
145 150 155 160

Trp Asp Thr Glu Pro Leu Gln Val Phe Val Val Pro His Ser His Asn
165 170 175

Asp Pro Gly Trp Leu Lys Thr Phe Asn Asp Tyr Phe Arg Asp Lys Thr
180 185 190

Gln Tyr Ile Phe Asn Asn Met Val Leu Lys Leu Lys Glu Asp Ser Arg
195 200 205

Arg Lys Phe Ile Trp Ser Glu Ile Ser Tyr Leu Ser Lys Trp Trp Asp
210 215 220

Ile Ile Asp Ile Gln Lys Lys Asp Ala Val Lys Ser Leu Ile Glu Asn
225 230 235 240

Gly Gln Leu Glu Ile Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala
245 250 255

Thr Pro His Tyr Phe Ala Leu Ile Asp Gln Leu Ile Glu Gly His Gln
260 265 270

Trp Leu Glu Asn Asn Ile Gly Val Lys Pro Arg Ser Gly Trp Ala Ile
275 280 285

Asp Pro Phe Gly His Ser Pro Thr Met Ala Tyr Leu Leu Asn Arg Ala
290 295 300

Gly Leu Ser His Met Leu Ile Gln Arg Val His Tyr Ala Val Lys Lys
305 310 315 320

His Phe Ala Leu His Lys Thr Leu Glu Phe Phe Trp Arg Gln Asn Trp
325 330 335

Asp Leu Gly Ser Val Thr Asp Ile Leu Cys His Met Met Pro Phe Tyr
340 345 350

Ser Tyr Asp Ile Pro His Thr Cys Gly Pro Asp Pro Lys Ile Cys Cys
355 360 365

Gln Phe Asp Phe Lys Arg Leu Pro Gly Gly Arg Phe Gly Cys Pro Trp
370 375 380

Gly Val Pro Pro Glu Thr Ile His Pro Gly Asn Val Gln Ser Arg Ala
385 390 395 400

Arg Met Leu Leu Asp Gln Tyr Arg Lys Lys Ser Lys Leu Phe Arg Thr
405 410 415

Lys Val Leu Leu Ala Pro Leu Gly Asp Asp Phe Arg Tyr Cys Glu Tyr
420 425 430

Thr Glu Trp Asp Leu Gln Phe Lys Asn Tyr Gln Gln Leu Phe Asp Tyr
435 440 445

Met Asn Ser Gln Ser Lys Phe Lys Val Lys Ile Gln Phe Gly Thr Leu
450 455 460

Ser Asp Phe Phe Asp Ala Leu Asp Lys Ala Asp Glu Thr Gln Arg Asp
465 470 475 480

Lys Gly Gln Ser Met Phe Pro Val Leu Ser Gly Asp Phe Phe Thr Tyr
485 490 495

Ala Asp Arg Asp Asp His Tyr Trp Ser Gly Tyr Phe Thr Ser Arg Pro
500 505 510

Phe Tyr Lys Arg Met Asp Arg Ile Met Glu Ser His Leu Arg Ala Ala
515 520 525

Glu Ile Leu Tyr Tyr Phe Ala Leu Arg Gln Ala His Lys Tyr Lys Ile
530 535 540

Asn Lys Phe Leu Ser Ser Ser Leu Tyr Thr Ala Leu Thr Glu Ala Arg
545 550 555 560

Arg Asn Leu Gly Leu Phe Gln His His Asp Ala Ile Thr Gly Thr Ala
565 570 575

Lys Asp Trp Val Val Val Asp Tyr Gly Thr Arg Leu Phe His Ser Leu
580 585 590

Met Val Leu Glu Lys Ile Ile Gly Asn Ser Ala Phe Leu Leu Ile Leu
595 600 605

Lys Asp Lys Leu Thr Tyr Asp Ser Tyr Ser Pro Asp Thr Phe Leu Glu
610 615 620

Met Asp Leu Lys Gln Lys Ser Gln Asp Ser Leu Pro Gln Lys Asn Ile
625 630 635 640

Ile Arg Leu Ser Ala Glu Pro Arg Tyr Leu Val Val Tyr Asn Pro Leu
645 650 655

Glu Gln Asp Arg Ile Ser Leu Val Ser Val Tyr Val Ser Ser Pro Thr
660 665 670

Val Gln Val Phe Ser Ala Ser Gly Lys Pro Val Glu Val Gln Val Ser
675 680 685

Ala Val Trp Asp Thr Ala Asn Thr Ile Ser Glu Thr Ala Tyr Glu Ile
690 695 700

Ser Phe Arg Ala His Ile Pro Pro Leu Gly Leu Lys Val Tyr Lys Ile
705 710 715 720

Leu Glu Ser Ala Ser Ser Asn Ser His Leu Ala Asp Tyr Val Leu Tyr
725 730 735

Lys Asn Lys Val Glu Asp Ser Gly Ile Phe Thr Ile Lys Asn Met Ile
740 745 750

Asn Thr Glu Glu Gly Ile Thr Leu Glu Asn Ser Phe Val Leu Leu Arg
755 760 765

Phe Asp Gln Thr Gly Leu Met Lys Gln Met Met Thr Lys Glu Asp Gly
770 775 780

Lys His His Glu Val Asn Val Gln Phe Ser Trp Tyr Gly Thr Thr Ile
785 790 795 800

Lys Arg Asp Lys Ser Gly Ala Tyr Leu Phe Leu Pro Asp Gly Asn Ala
805 810 815

Lys Pro Tyr Val Tyr Thr Thr Pro Pro Phe Val Arg Val Thr His Gly
820 825 830

Arg Ile Tyr Ser Glu Val Thr Cys Phe Phe Asp His Val Thr His Arg
835 840 845

Val Arg Leu Tyr His Ile Gln Gly Ile Glu Gly Gln Ser Val Glu Val
850 855 860

Ser Asn Ile Val Asp Ile Arg Lys Val Tyr Asn Arg Glu Ile Ala Met
865 870 875 880

Lys Ile Ser Ser Asp Ile Lys Ser Gln Asn Arg Phe Tyr Thr Asp Leu
885 890 895

Asn Gly Tyr Gln Ile Gln Pro Arg Met Thr Leu Ser Lys Leu Pro Leu
900 905 910

Gln Ala Asn Val Tyr Pro Met Thr Thr Met Ala Tyr Ile Gln Asp Ala
915 920 925

Lys His Arg Leu Thr Leu Leu Ser Ala Gln Ser Leu Gly Val Ser Ser
930 935 940

Leu Asn Ser Gly Gln Ile Glu Val Ile Met Asp Arg Arg Leu Met Gln
945 950 955 960

Asp Asp Asn Arg Gly Leu Glu Gln Gly Ile Gln Asp Asn Lys Ile Thr
965 970 975

Ala Asn Leu Phe Arg Ile Leu Leu Glu Lys Arg Ser Ala Val Asn Thr
980 985 990

Glu Glu Glu Lys Lys Ser Val Ser Tyr Pro Ser Leu Leu Ser His Ile
995 1000 1005

Thr Ser Ser Leu Met Asn His Pro Val Ile Pro Met Ala Asn Lys
1010 1015 1020

Phe Phe Ser Pro Thr Leu Glu Leu Gln Gly Glu Phe Ser Pro Leu
1025 1030 1035

Gln Ser Ser Leu Pro Cys Asp Ile His Leu Val Asn Leu Arg Thr
1040 1045 1050

Ile Gln Ser Lys Val Gly Asn Gly His Ser Asn Glu Ala Ala Leu
1055 1060 1065

Ile Leu His Arg Lys Gly Phe Asp Cys Arg Phe Ser Ser Lys Gly
1070 1075 1080

Thr Gly Leu Phe Cys Ser Thr Thr Gln Gly Lys Ile Leu Val Gln
1085 1090 1095

Lys Leu Leu Asn Lys Phe Ile Val Glu Ser Leu Thr Pro Ser Ser
1100 1105 1110

Leu Ser Leu Met His Ser Pro Pro Gly Thr Gln Asn Ile Ser Glu
1115 1120 1125

Ile Asn Leu Ser Pro Met Glu Ile Ser Thr Phe Arg Ile Gln Leu
1130 1135 1140

Arg

<210> 19
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of ManII-GalT

<400> 19
atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
tcgctctacc tgatgctgga ccggggtcac ttagactacc ccaggaaccc gcgcgcgag 120
ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
ttgctagctg agaataatga gatcatctca aatatttagag actcagtcat caatttgagt 240
gagtcgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctggctca 300
cccgccctgcc ctgaggagtc cccgctgctt gtggccccca tgctgattga gtttaacatg 360
cctgtggacc tggagctcgt ggcaaagcag aacccaaatg tgaagatggg cggccgctat 420
gccccccaggg actgcgtctc tcctcacaag gtggccatca tcattccatt ccgcaaccgg 480
caggagcacc tcaagtactg gctatattat ttgcacccag tcctgcagcg ccagcagctg 540
gactatggca tctatgttat caaccaggcg ggagacacta tattcaatcg tgctaagctc 600
ctcaatgttg gctttcaaga agccttgaag gactatgact acacctgctt tgtgttttagt 660
gacgtggacc tcattccaat gaatgaccat aatgcgtaca ggtgttttc acagccacgg 720
cacatttccg ttgcaatgga taagtttggaa ttcaagctac cttatgttca gtatttggaa 780
ggtgtctctg ctctaagtaa acaacagttt ctaaccatca atggatttcc taataattat 840
tggggctggg gaggagaaga tgatgacatt tttaacagat tagtttttag aggcattgtct 900
atatctcgcc caaatgctgt ggtcgaggagg tgtcgcattca tccgcccactc aagagacaaa 960

aaaaatgaac ccaatcctca gaggttgac cgaattgcac acacaaggaa gacaatgctc	1020
tctgatggtt tgaactcaact cacctaccag gtgctggatg tacagagata cccattgtat	1080
acccaaatca cagtggacat cgggacacccg agctag	1116

<210> 20
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of ManII-GalT

<400> 20

Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys			
1	5	10	15

Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp		
20	25	30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu		
35	40	45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu		
50	55	60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser			
65	70	75	80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln		
85	90	95

Gly Ala Gly Ser Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly		
100	105	110

Pro Met Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala		
115	120	125

Lys Gln Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp		
130	135	140

Cys Val Ser Pro His Lys Val Ala Ile Ile Pro Phe Arg Asn Arg			
145	150	155	160

Gln Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln		
165	170	175

Arg Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp

180

185

190

Thr Ile Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala
195 200 205

Leu Lys Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu
210 215 220

Ile Pro Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg
225 230 235 240

His Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val
245 250 255

Gln Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr
260 265 270

Ile Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp
275 280 285

Asp Ile Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro
290 295 300

Asn Ala Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys
305 310 315 320

Lys Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys
325 330 335

Glu Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu
340 345 350

Asp Val Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly
355 360 365

Thr Pro Ser
370